SIR epidemics on random graphs with clustering[a]

Carolina Fransson
Stockholm University
carolina.fransson@math.su.se

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[a] This presentation is based on a master's project under the supervision of Dr. Pieter Trapman.

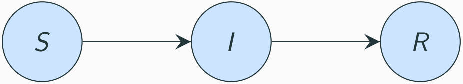
Some questions of interest in epidemic modelling:

1. What is the impact of the underlying social network on the spread of the disease?
2. What is the probability of a large outbreak?
3. If a major outbreak occurs, how large will it be?
4. What control measures (e.g. vaccination) are necessary to contain the disease?

The SIR model

At each time point, individuals are divided into three groups according to health status:

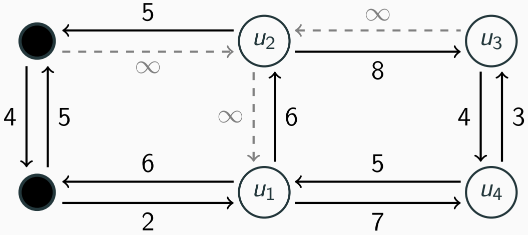
- S - Susceptible
- I - Infectious
- R - Recovered



Graph representation of an epidemic

A social network can be represented by a directed graph:

- Nodes represent individuals
- Edges represent relationships
- Edge weights represent times of transmission



Reproduction numbers

- Basic reproduction number R_0
- Expected number of cases caused by a "typical" infected during the early phase
- Threshold properties: $R_0 \leq 1 \iff$ major outbreak not possible
  $R_0 > 1 \iff$ major outbreak might occur
- Preventive/control measures: For simple models, a fraction

$$1 - \frac{1}{R_0}$$

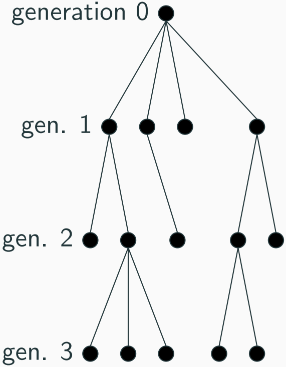
  has to be vaccinated with a perfect vaccine to "surely" prevent a major outbreak

Estimated values of R_0 for the 2014 Ebola outbreak with 95% confidence intervals:

Guinea	Sierra Leone	Liberia
1.51 (1.50-1.52)	2.53 (2.41-2.67)	1.59 (1.57-1.60)

Multi-type Galton-Watson processes

- $s \in \mathbb{N}$ types of individuals
- Individuals reproduce independently at age 1, offspring distribution determined by type
- Mean matrix $M = (m_{ij})_{i,j}^{s}$
- m_{ij}: expected number of type j individuals produced by a type i indvidual



Perron-Frobenius theorem

Let M be positively regular. Then M has a dominant, real-valued, simple eigenvalue $r > 0$, and there exists vectors $\bar{u}, \bar{v}$ with strictly positive coordinates such that

$$M\bar{u} = r\bar{u} \text{ and } \bar{v}'M = r\bar{v}'.$$

If $\bar{u}$ and $\bar{v}$ are normalized, so that $\bar{u}' \cdot \bar{1} = \bar{v}' \cdot \bar{u} = 1$, then

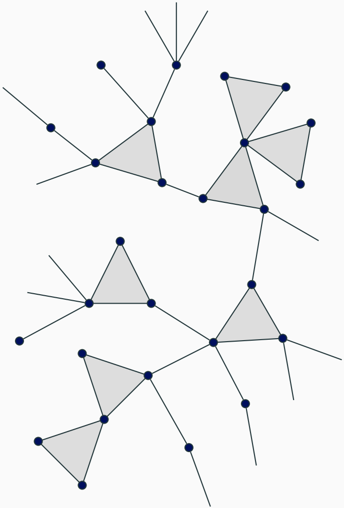
$$\frac{1}{r^k} M^k \to \bar{u}\bar{v}'$$

as $k \to \infty$.

- Let the vector Z_k denote the number of realized individuals individuals of generation k, then $E(Z_k|Z_0) = (M^k)'Z_0$
- r has the threshhold properties of R_0
- $r = R_0$

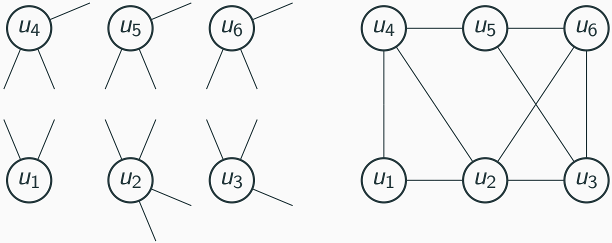
Clustering

- A graph exhibits clustering if it contains a high amount of triangles.
- The friends of an individual tends to be friends as well
- Why are short cycles a problem?
  - Branching process approximations



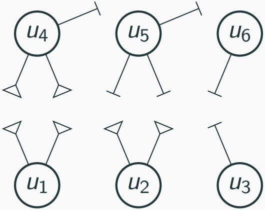
Configuration model

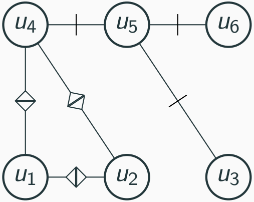
1. Start with N nodes
2. Assign a degree (number of half-edges) to each node
3. Match the half-edges uniformly at random



Configuration model with clustering

- Miller (2009) and Newman (2009)
- Two types of edges: single edges and triangle edges
    1. Start with N nodes
    2. Assign two degrees to each node, a single degree and a triangle degree
    3. Match the half-edges uniformly at random

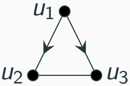




Previous results

Miller (2009):

- Disease transmitted along each edge with fixed probability T, independently
- Discrete time
- Attributes secondary and tertiary cases in a triangle to primary case.



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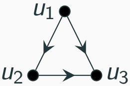

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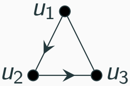

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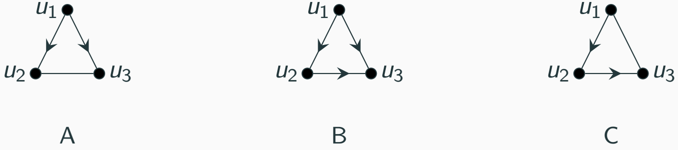
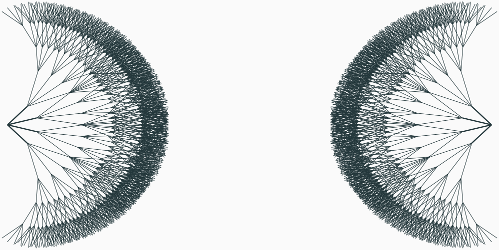
An SIR model with heterogeneous infectivity

- Underlying social network: configuration graph with clustering
- I.i.d. node weights $\{T_i\}_i$:

$$P(u_i \text{ infects neighbour } u_j | T_i) = T_i$$



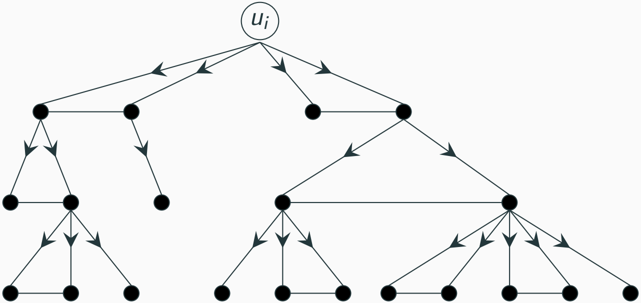
- Special case: I.i.d. infectious periods, individuals make contact with each neighbour independently at Poisson rate 1



- Sequence $(E_N)_N$ of epidemic processes, where N denotes the population size
- Construct coupling of $(E_N)_N$ and suitable branching processes:
  - Forward branching processes - ancestor(s) corresponds to initial case(s)
  - Backward branching processes - for each individual u, we explore the individuals that would transmit the disease to u
- u contracts the disease if the backward process connects with the forward process
- u does not contract the disease if the backward process goes extinct

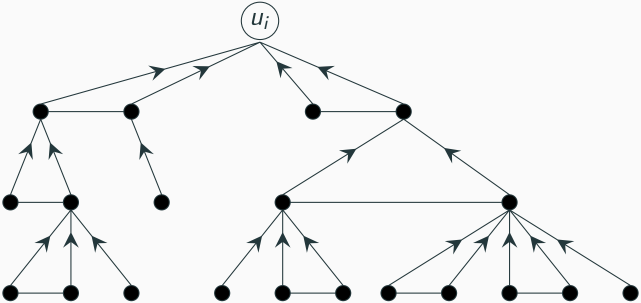
Branching process approximation - forward process

Probability of extinction ≈ probability of minor outbreak



Branching process approximation - backward process

Probability of non-extinction ≈ expected fraction infected, given that a major outbreak occurs



N: population size

q: extinction probability of the approximating forward branching processes

q_b: extinction probability of the approximating backward branching processes

$\mathcal{S}_N$: the fraction that ultimately escapes infection

Size of a major outbreak

$$S_N \xrightarrow{d} S$$

as $N \to \infty$ where

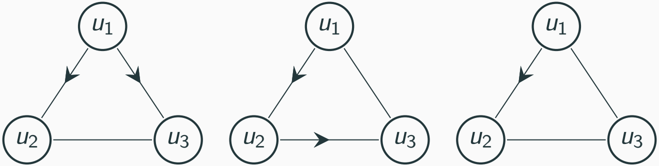
$$S = \begin{cases} 1 & w.p.\ 1-q \\ q_b & w.p.\ q \end{cases}$$

The forward process

Type I: Infected along a triangle edge, brother not susceptible

Type II: Infected along a triangle edge, brother susceptible

Type III: Infected along a single edge

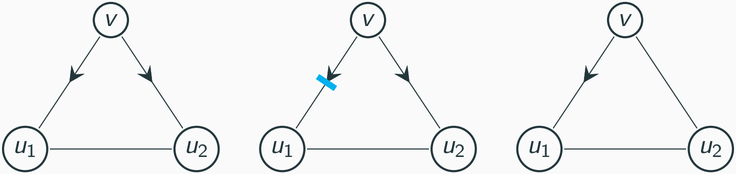


Conditioning on the transmission weights and using conditional independence gives R_0 and the probability of a major outbreak

Vaccination - forward process

Fraction f_v of population vaccinated with perfect (provides full and permanent immunity) vaccine

Type I: Infected along triangle edge, brother not susceptible
Type II: Infected along triangle edge, brother might be susceptible
Type III: Infected along single edge



f_v : fraction vaccinated
M_v: mean matrix
M: mean matrix if $f_v = 0$

$$M_v = (1 - f_v)M$$

Thank you for your attention!

- Althaus CL (2014). "Estimating the Reproduction Number of Ebola Virus (EBOV) During the 2014 Outbreak in West Africa". PLOS Currents Outbreaks.
- Miller, Joel (2009). "Percolation and epidemics in random clustered networks". Phys. Rev.
- Newman, Mark (2009). "Random Graphs with Clustering". Phys. Rev.